

M A S L D R V K V L V L G D S  
 AGGGAAGCCAGTGGCAAG ATG GCG TCC CTG GAT CGG GTG AAG GTA CTG GTG TTG GGA GAC TCA SEQ ID NO:2  
 ↑SEQ ID NO:3↓  
 G V G K S S L V H L L C Q N Q V L G N F 35  
 GGT GTT GGG AAA TCT TCG TTA GTC CAT CTC CTA TGC CAA AAT CAA GTG CTG GGA AAT CCA 105  
 S W T V G C S V D V R V H D Y K E G T F 55  
 TCA TGG ACT GTG GGC TGC TCA GTG GAT GTC AGA GTT CAT GAT TAC AAA GAA GGA ACC CCA 165  
 E E K T Y Y I E L W D V G G S V G S A S 75  
 GAA GAG AAG ACC TAC TAC ACA GAA TTA TGG GAT GTT GGA GGC TCT GTG GGC AGT GCC AGC 225  
 S V K S T R A V F Y N S V N G I I F V H 95  
 AGC GTG AAA AGC ACA AGA GCA GTA TTC TAC AAC TCC GTA AAT GGT ATT ATT TTC GTA CAC 285  
 D L T N K K S S Q N L R R W S L E A L N 115  
 GAC TTA ACA AAT AAG AAG TCC TCC CAA AAC TTG CGT CGT TGG TCA TTG GAA GCT CTC AAC 345  
 R D L V P T G V L V T N G D Y D Q E Q F 135  
 AGG GAT TTG GTG CCA ACT GGA GTC TTG GTG ACA AAT GGG GAT TAT GAT CAA GAA CAG TTT 405  
 A D N Q I P L L V I G T K L D Q I H E T 155  
 GCT GAT AAC CAA ATA CCA CTG TTG GTA ATA GGG ACT AAA CTG GAC CAG ATT CAT GAA ACA 465  
 K R H E V L T R T A F L A E D F N P E E 175  
 AAG CGC CAT GAA GTT TTA ACT AGG ACT GCT TTC CTG GCT GAG GAT TTC AAT CCA GAA GAA 525  
 I N L D C T N P R Y L A A G S S N A V K 195  
 ATT AAT TTG GAC TGC ACA AAT CCA CGG TAC TTA GCT GCA GGT TCT TCC AAT GCT GTC AAG 585  
 L S R F F D K V I E K R Y F L R E G N Q 215  
 CTC AGT AGG TTT TTT GAT AAG GTC ATA GAG AAG AGA TAC TTT TTA AGA GAA GGT AAT CAG 645  
 I P G F P D R K R F G A G T L K S L H Y 235  
 ATT CCA GGC TTT CCT GAT CGG AAA AGA TTT GGG GCA GGA ACA TTA AAG AGC CTT CAT TAT 705  
 D 237  
 GAC TGA 711  
 ←SEQ ID NO:3↑  
 ATTACACTCATCCTTTGGAAGAGTGAGCAAGCAGTGGCAGTTTTTCACAGCTCATCTTGCTGTGTTCATTATTACCAT  
 CACAGCCTTTTAACAAAATCATCTTAAATGCTACCCCTTCAGCCTTACCCTTTAATGGAAAAATGAAAGGAAGTGACAA  
 TACGGGAGGTCCAAACTTTGTCCCTGTTCTCTGTGTTCCTTACCTTCTGTCCCTGTGTATAGATTATGTAAAGCCTT  
 GTGTAAATATGAGATGTTGTCAAAATGATGCAGTAAATGAGCAATGACAGTGTACTGCAGAGAAAATTTACTCTTGCCCT  
 AGAACTGGAGGGTTTTATGGGTCTGTAATTTTCCACACTCATTGCTGAAAGCTTAATTAAGTACTTCAAAAACGTAT  
 CTCCATTGTTTTACCTTCTTGAGGGGAACGGTCTGTGTTAACCAGCCCTGAGTTGTCTACCCCAACCAATCTCTGTCAAT  
 TTCAAAGATGCAPAAATGGTGTATTTAATTGTCTCCACCATTGTACACACAGGAATGCCTAATAATAGCAACCCCTGT  
 CTCCCTCTCTCTCCTTTGCAATGGCTCAGTGACTGGAAGAGCGGACTAATAGCCAGAGTTAAATATAAATACAAAT

FIG. 1A

Title: 47324, A NOVEL HUMAN G-PROTEIN AND USES THEREFOR

Inventor: Rachel Meyers

Application No.: To be Assigned

Docket No.: 381552003500

Sheet 2 of 6

TAATAATACATAGAGAACAGCAATACCAGAAAAAAGAATTCTGGTAAAATGATGTGAAAAATTGACAGCTCCCTCACT  
CTTAAGGTTGCTGCTATATACAGTCTAGGTTTTCTGTTTGAAATAGGTAGGGTAAATCTAAGACCTGCACAAGGGCA  
GTGAGAGACATTTACAGCCTCCTCTCTATTTGTTTTTTAAGGAAAAGTCAACTCCTGAAATGTCCCTTAGCTATAATC  
AGAAAATAAGAATATTATTCTGTGTCAACAATGTATTTATGGAGAGAAGTAAAAATAAGTTCCACAGCAACACAAAAA  
CATGAATTATTGAACTA

0045473-0000  
FIG. 1B

FIG. 1B

107653 E2T5H660

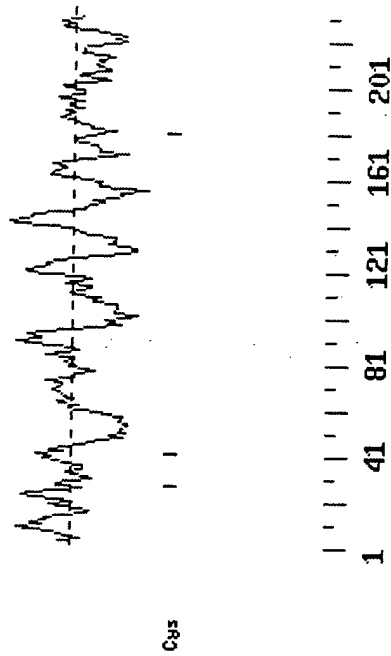


FIG. 2

FIG. 3

FIG. 4

Query: 35 PSWTV-GCSVDVRVHDYKEGTPEEKT--YYIELWDXXXXXXXXXXXXXTRAVFYNSVNGI 91  
 P+WT S D + Y TP Y++E +D R FY +++GI  
 Sbjct: 69 PTWTTTPSSSEDSENYPYMRSTPTTTNILYFVEFYDLNSDWRMCRQQ---RESFYKNIDGI 125 SEQ ID  
 NO:6

Query: 92 IFVHDLTNKKSSQNLRWSLEALNRDLVPTGVLVTNGDYDQEQFADNQIPLLIVIGTKLDQ 151  
 + V+++ S +L W + L + + + + P+LV+GT LD+  
 Sbjct: 126 VLVYNMLELSSQDSLHDWLYDPLRQICKHRHLRI-----RSILKNHNAPILVVGTNLDK 179

Query: 152 IHETKRHEVLTRTAFLAEDFNPEEINLDCTNPRYLAAGSSNAVKLSRFFDKVIE-KRYF 209  
 + L R +A N EE+ ++C +P+ S N KL F ++VIE K F  
 Sbjct: 180 L---MRRPLRRRGSIAHQNLNVEEMLVNCCLDPQSFVDKSRNQGLYGLNRVIEFKEQF 234

FIG. 5a

Query: 7 VKVLVLGDSGVGKSSLVHLLCQNVLGNP-SWTVG---CSVDVRVHDYKE 52  
 V++L+LGD GVGK+SL +L+ ++ P S TVG V VR+H+Y +  
 Sbjct: 12 VRILMLGDRGVGKTSLTNLMATTEITPTPDSRTVGEESWHVQVRLHEYSK 61 SEQ ID NO:7

FIG. 5b

Query: 121 TGVLVTNGD--YDQEQFAD-NQIPLLIVIGTKLDQIHETKRHEVL--TRTAFLAEDFNPEE 175  
 T L T+G +D E+F Q P+LV+GTKLD + E KRH + + +A+ EE  
 Sbjct: 19 TDNLGTDGHILFDMEEFLGATQTPILVMGTKLDLLDE-KRHPKMGVKKPGGIADKCGAEE 77 SEQ ID  
 NO:8

Query: 176 INLDCTNPRYLAAGSSNAVKLSRFFDKVIEKRYFLR-----EGNQIPGFPDRKRFGAG 228  
 I L+C N R LAAG+++AVKLSRFFD+VIE R LR + PDR+RFG  
 Sbjct: 78 IWLNCNRSRLAAGTTDAVKLSRFFDRVIENRKALRAALAFGVSSSNVSPDRRRFGPT 137

Query: 229 TLK 231  
 + K  
 Sbjct: 138 SAK 140

FIG. 6

47324, A NOVEL HUMAN G-PROTEIN AND USES THEREFOR

Query: 6 RVKVLVLGDSGVGKSSLVHLLCQNQVLGNPSWTVGCSVDVRVHDYKEGTPEEKTYIE 63  
+V+VLV+GDSGVGK+SLVHL+ + + P T+GC+V V+ Y G+P + I+  
Sbjct: 80 QVRVLVVGDSGVGKTSLVHLINKGSSIVRPPQTIGCTVGVKHITY--GSPASSSSSIQ 135 SEQ ID NO:9

FIG. 7

Query: 8 KVLVLGDSGVGKSSLVHLL--CQNQ-----VLGNPSWTVGCSVDVRVHDYKEGT 54  
K++++GDSGVGK+SL++ L +N V+ + T+G +V+ T  
Sbjct: 7 KIVIIGDSGVGKTSLLNKLRFTEENSFTEEDPTTRTVDSYKSTIGVDFNVKTTIEVVD 66 SEQ ID  
NO:10

Query: 55 PEEKTYIIELDWXXXXXXXXXXXXXTRAVFNSVNGIIFVHDLTNKKSS-QNLRRWSLEA 113  
+ K +++WD A +Y I V+D+ + +SS +N +W E  
Sbjct: 67 -DGKNIKLQIWDTAGQERYRSMLEA-YRGAEADIIVDVDSSESSFENQTKWLKEI 124

Query: 114 LNRDLVPTGVLVTNGDYDQEQFADNQIPLLVIGTKLD-QI---HETKRHEVLTRTAFLAE 169  
L +N E+ ++N +P+++G K D ++ E + + T A+  
Sbjct: 125 LRH-----ASN-----EEASEN-VPIILVGKNKADLEVPNPPEVEEEKEEASTEEEAQ 170

Query: 170 DFNPEEINLDCTNPRYLAAGSSNAVKLSRFFDKVIEKRYFLREGNQIPGFPDRKRF 225  
F EE L P + + + F +++ R L++ +I D++++  
Sbjct: 171 SF-AEEKGLGVV-PFIETSAKTTGTNVEEVFQELV--REILKKKKEIQEKADQEKY 222

FIG. 8

FIG. 7